

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 14:04:54 ; Search time 1 Seconds

(without alignments)  
6.964 Million cell updates/sec

Title: us-09-944-896-49

Perfect score: 1876

Sequence: 1 cctcttgcacacagccca.....tcagctgaataaaaaaa 1876

Scoring table: IDENTITY-NIC

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1856 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : seq264-1.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match length DB ID Description

1 1764.5 94.1 1856 1 us-09-790-264-1

2 25.8 1.4 1856 1 us-09-790-264-1

ALIGNMENTS

Query Match 94.1%; Score 1764.5; DB 1; Length 1856;

Best Local Similarity 98.0%; Pred. No. 0;

Matches 1794; Conservative 0; Mismatches 10; Indels 27; Gaps 1;

46 GCTCCATCCAGCCCTGGAAGAACAGCCGGGTGGTGGAGCCAGCTGTGACGAGACCTG 105

18 GCTCCATCCAGCCCTGGAAGAACAGCCGGGTGGTGGAGCCAGCTGTGACGAGACCTG 77

106 ACGGGCCCAACAGACCCATGCTGATCCAGAGACCTCCCTGGCCGGGGGCACTCTGG 165

78 ACGGGCCCAACAGACCCATGCTGATCCAGAGACCTCCCTGGCCGGGGGCACTCTGG 137

166 CTGTGCTCTGAGCCCTCTTGGACACCACTGGGAGAGGTGTGGCCACCCAGCTGAG 225

138 CTGTGCTCTGAGCCCTCTTGGACACCACTGGGAGAGGTGTGGCCACCCAGCTGAG 197

226 AGCAGGCTCGAGTGGCGGAGCCCTGAAACAGAGAGTTTCTTGTCTCTCCCTGC 285

198 AGCAGGCTCGAGTGGCGGAGCCCTGAAACAGAGAGTTTCTTGTCTCTCCCTGC 257

286 ACAACCGCTGCGACAGCTGGGTCCAGCCCTTGGGGTGAATGCGAGAGGTGAGCTGA 345

258 ACAACCGCTGCGACAGCTGGGTCCAGCCCTTGGGGTGAATGCGAGAGGTGAGCTGA 317

Sequence Alignment

QY 346 GTGACAGCGCTGGCCCACTGCTCAAGCCAGGGGACCCCTGTGTGAATCCCAACCCCGA 405

DB 318 GTGACAGCGCTGGCCCACTGCTCAAGCCAGGGGACCCCTGTGTGAATCCCAACCCCGA 377

QY 406 GCTTGACATCGGCTGTGGGACCCCTGGAAGTGGGCTGGAAATCATGAGTGTGCGCG 465

DB 378 GCTTGACATCGGCTGTGGGACCCCTGGAAGTGGGCTGGAAATCATGAGTGTGCGCG 437

QY 466 CGGCTTGGCTCTTGTGAAGTGTGACGCTTATGTTGGAGAGGGGACGCTGACA 525

DB 438 CGGCTTGGCTCTTGTGAAGTGTGACGCTTATGTTGGAGAGGGGACGCTGACA 497

QY 526 GCCACGCGGACGAGAGTGTGCTGGCAAGCCCACTGCAACCCATACAGCAGCTGTGT 585

DB 498 GCCACGCGGACGAGAGTGTGCTGGCAAGCCCACTGCAACCCATACAGCAGCTGTGT 557

QY 586 GGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGACCTGTGCTGCAAGGCGCAGACGA 645

DB 558 GGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGACCTGTGCTGCAAGGCGCAGACGA 617

QY 646 TAGAAGCTTGTCTGTGCTACTCCCCGGAGGCACTGGAGGTCAACGGGAGACAA 705

DB 618 TAGAAGCTTGTCTGTGCTACTCCCCGGAGGCACTGGAGGTCAACGGGAGACAA 677

QY 706 TCATCCCTTATAGAAGAGGTGCTGTGCTGTGCTGCAAGCAGCTGTGCTGCTGT 765

DB 678 TCATCCCTTATAGAAGAGGTGCTGTGCTGTGCTGCAAGCAGCTGTGCTGCTGT 737

QY 766 TCAGAGCTGGAGACCTGAGGGGCTGTGTGAGGTGCTGCTGCAAGCAGCTGTGCTGCT 825

DB 738 TCAGAGCTGGAGACCTGAGGGGCTGTGTGAGGTGCTGCTGCAAGCAGCTGTGCTGCT 797

QY 826 GCTGCGAAGCAATGAGAGCTGCTCAACATCAGACCTGCTGCTGCTGCTGCTGCT 885

DB 798 GCTGCGAAGCAATGAGAGCTGCTCAACATCAGACCTGCTGCTGCTGCTGCTGCT 857

QY 886 ACACGGGACAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 945

DB 858 ACACGGGACAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 917

QY 946 AGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005

DB 918 AGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 977

QY 1006 TGCAATTTCCCTTCCACACCTGAGCTGAGAGTGAAGAGTGTGCTGCTGCTGCT 1065

DB 978 TGCAATTTCCCTTCCACACCTGAGCTGAGAGTGAAGAGTGTGCTGCTGCTGCT 1037

QY 1066 CAGAGGACAGACCTTATACAGAGCCAGATGAATGCAAGGAAAGCGGGGCTGAG 1125

DB 1038 CAGAGGACAGACCTTATACAGAGCCAGATGAATGCAAGGAAAGCGGGGCTGAG 1097

QY 1126 CCGAGATCAAGACCCAGAAAGTGCAGACATCTGCTGCTTATCTGAGGCGCTGAGA 1185

DB 1098 CCGAGATCAAGACCCAGAAAGTGCAGACATCTGCTGCTTATCTGAGGCGCTGAGA 1157

QY 1186 CCACCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1245

DB 1158 CCACCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1217

QY 1246 ACAAGACCGCAAGGACTCTTCCGCTGGGCAAGAGGAGACACAGGCTTCAACAGTT 1305

DB 1218 ACAAGACCGCAAGGACTCTTCCGCTGGGCAAGAGGAGACACAGGCTTCAACAGTT 1277

QY 1306 TTGCTTTGGGAGCGCTGCAACAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1365

DB 1278 TTGCTTTGGGAGCGCTGCAACAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1310

QY 1366 GCAACTGCTGAGCTGAGGCTTCAAGTGTGCTTCAACTGGAAGACAGGCTGCAAAA 1425

DB 1311 GCAACTGCTGAGCTGAGGCTTCAAGTGTGCTTCAACTGGAAGACAGGCTGCAAAA 1370

```
QY 1426 CCCGAAACCGTTACATCTGCCAGTTTGGCCAGAGACATCTCCCGGTGGGCCCAAGGTT 1485
    |||||||
DB 1371 CCCGAAACCGTTACATCTGCCAGTTTGGCCAGAGACATCTCCCGGTGGGCCCAAGGTT 1430
    |||||||
QY 1486 CCTGAGGCCCTGACCAATGGCTCCCTGCGCCCTGGGAGACCGGCTCTGCTTACCTG 1545
    |||||||
DB 1431 CCTGAGGCCCTGACCAATGGCTCCCTGCGCCCTGGGAGACCGGCTCTGCTTACCTG 1490
    |||||||
QY 1546 TCTGCCACCTGTCTGGAACAAGGCCAGTTAAGACCAATGCTCATGTCCAAAGAG 1605
    |||||||
DB 1491 TCGGCCACCTGTCTGGAACAAGGCCAGTTAAGACCAATGCTCATGTCCAAAGAG 1550
    |||||||
QY 1606 TCTCAGACCTTGCACATGCCAGAGATTGGGCAAGAGAGAGGCGAGGCGAGTGAAGGC 1665
    |||||||
DB 1551 TCTCAGACCTTGCACATGCCAGAGATTGGGCAAGAGAGAGGCGAGGCGAGTGAAGGC 1610
    |||||||
QY 1666 CAGGAGGTGAGTGTAGAAAGCTGGGGCCCTTGCCTGCTTTTGTATTGGGAAGATGGG 1725
    |||||||
DB 1611 CAGGAGGTGAGTGTAGAAAGCTGGGGCCCTTGCCTGCTTTTGTATTGGGAAGATGGG 1670
    |||||||
QY 1726 CTTCATTTAGATGGCGAAGAGAGACACCGCCAGTGTCCAAAAAGGCTGCTCTTCC 1785
    |||||||
DB 1671 CTTCATTTAGATGGCGAAGAGAGACACCGCCAGTGTCCAAAAAGGCTGCTCTTCC 1730
    |||||||
QY 1786 ACCTGGCCCAACCTCTGGGGGCAAGCGAGCTTCCCTGGCATGAACCCACGGGGTAT 1845
    |||||||
DB 1731 ACCTGGCCCAACCTCTGGGGGCAAGCGAGCTTCCCTGGCATGAACCCACGGGGTAT 1790
    |||||||
QY 1846 TAAATTATGATCAGCTGAAAAA 1876
    |||||||
DB 1791 TAAATTATGATCAGCTGAAAAA 1821
    |||||||
```

RESULT 2  
us-09-790-264-1/c

Query Match 1.4%: Score 25.8; DB 1; Length 1856;  
Best Local Similarity 67.9%; Pred. No. 0;  
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

```
QY 1124 GGCCCAATCAAGACCAAGAAAGTCAGAGACATCTGCTTATCTGGGCC 1176
    |||||||
DB 1148 GGCCCAATCAAGACCAAGAAAGTCAGAGATGCTCTGACCTTCTGGCTGATCTGGGCC 1096
    |||||||
```

Search completed: September 17, 2003, 14:04:57  
Job time : 2 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 17, 2003, 14:00:33 ; Search time 0.001 seconds  
(without alignments)  
202.930 Million cell updates/sec

Title: us-09-944-896-50

Perfect score: 2529

Sequence: 1 MLHPETSPGRGHLAVLAL.....RNRYICQFAOEHSRMGPGS 455

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 446 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : seq264-2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description     |
|------------|--------|-------------|--------|----|-----------------|
| 1          | 2447.5 | 96.8        | 446    | 1  | us-09-790-264-2 |

#### ALIGNMENTS

RESULT 1  
us-09-790-264-2

Query Match 96.8%; Score 2447.5; DB 1; Length 446;

Best Local Similarity 97.1%; Pred. No. 0;

Matches 442; Conservative 1; Mismatches 3; Indels 9; Gaps 1;

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | MLHPETSPGRGHLAVLALIGTWAEEVWPPOLOEQAPMAGALNRRKESFLLSLNRLRS  | 60  |
| DB | 1   | MLHPETSPGRGHLAVLALIGTWAEEVWPPOLOEQAPMAGALNRRKESFLLSLNRLRS  | 60  |
| QY | 61  | WVOPPADMRRLDMSDSLQALQARALCGIPTPSIASGLWRTLOYGMNOLLPGIASF    | 120 |
| DB | 61  | WVOPPADMRRLDMSDSLQALQARALCGIPTPSIASGLWRTLOYGMNOLLPGIASF    | 120 |
| QY | 121 | VEVYSLMEFAGGORYSHAGECARNATCTHYTLWATSSQLCGRHLCSAGQTAIEAFVC  | 180 |
| DB | 121 | VEVYSLMEFAGGORYSHAGECARNATCTHYTLWATSSQLCGRHLCSAGQTAIEAFVC  | 180 |
| QY | 181 | AYSPGNGMEVNGKTIIPYKKGAMCSLCTASVSGCFKAMDHAGGLCEVPRNRCMSQNHG | 240 |
| DB | 181 | AYSPGNGMEVNGKTIIPYKKGAMCSLCTASVSGCFKAMDHAGGLCEVPRNRCMSQNHG | 240 |
| QY | 241 | RLNISTCHCHCPPGYTGRCYQVRCSLQCVHGRFREECSCYCDIGYGAGCATKVHFPFH | 300 |
| DB | 241 | RLNISTCHCHCPPGYTGRCYQVRCSLQCVHGRFREECSCYCDIGYGAGCATKVHFPFH | 300 |

|    |     |   |     |
|----|-----|---|-----|
| QY | 301 | TCDLRIDGCFMYSSSEADTYRRAMKQGRGVLAQIKSOKVODILAFYLRLETTNEVT  | 360 |
| DB | 301 | TCDLRIDGCFMYSSSEADTYRRAMKQGRGVLAQIKSOKVODILAFYLRLETTNEVT  | 360 |
| QY | 361 | DSDFETRNFWIGLTYRTAKDSFRWANGEHQAFTSFAFGOPDNHGLVLSAMFGNCVEL | 420 |
| DB | 361 | DSDFETRNFWIGLTYRTAKDSFRWANGEHQAFTSFAFGOPDNHGLVLSAMFGNCVEL | 420 |
| QY | 421 | QASAFNMNDQRCRTNRNYICQFAOEHSRMGPGS 455                     |     |
| DB | 412 | QASAFNMNDQRCRTNRNYICQFAOEHSRMGPGS 446                     |     |

Search completed: September 17, 2003, 14:00:33  
Job time : 0.001 secs

